

SEQUENCE LISTINGS

<110> INJE UNIVERSITY

<120> CANCER CELL TARGETING GENE DELIVERY METHOD

<130> Q94769

<150> KR 10-2003-0079897

<151> 1003-11-12

<150> PCT/KR2004/000545

<151> 2004-03-15

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<213> Artificial Sequence

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<223> Env F primer

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<223> 597LN primer

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 <223> Spike R2 primer

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 <223> LnkNScFv primer

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 <212> DNA
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<223> ScFvLnkC primer

<400> 6

actgcctcct ccacctgagg cgggggtgaa gtccca

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<210> 7

<211> 2058

<212> DNA

<213> SEATO type of GaLV Env glycoprotein

<220>

<221> sig_peptide

<222> (1)..(126)

<220>

<221> misc_feature

<222> (127)..(1467)

<223> surface subunit region

<220>

<221> misc_feature

<222> (1468)..(2025)

<223> transmembrane domain

<400> 7

atggtattgc tgcctgggtc catgcttctc acctcaaacc tgcaccacct tcggcaccag 60

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gggacgagtc tgcaaaataa gaacccccac cagcccatga ccctcacttg gcaggtactg 180

tcccaaactg gagacgttgt ctgggataca aaggcagtc agcccccttg gacttggtgg 240

cccacactta aacctgatgt atgtgccttg gcggttagtc ttgagtcctg ggatatcccg 300

ggaaccgatg tctcgtcttc taaacgagtc agacctccgg actcagacta tactgccgct 360

tataagcaaa tcacctgggg agccataggg tgcagctacc ctctgggctag gactagaatg 420

gcaagctcta ccttctacgt atgtccccgg gatggccgga ccctttcaga agctagaagg	480
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gaagagtgct gtttttacat agaccactca ggtgcaglac gggactccat gaaaaaactc 1800
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 ctctccttc tgttgctcat cctcgggcca tgcataatca ataagttagt tcaattcatc 1980
 aatgatagga taagtgcagt taaaattctg gtccttagac aaaaatatca ggccctagag 2040
 aacgaaggta acctttaa 2058

<210> 8
 <211> 786
 <212> DNA
 <213> Tag-72pS1

<220>
 <221> misc_feature
 <222> (346)..(390)
 <223> (Gly4Ser)3 linker

<220>
 <221> misc_feature
 <222> (739)..(777)
 <223> PreS1 Tag

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 tcccagaagt tccaggagcg cgtgacaatc actgcagaca aatccgagag cacagcctac 240
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 aacatggcat actggggcca agggactctg gtcactgtct cttcagggtg aggcggttca 360

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 tacagcagca acaataagaa ctacttagct tggtagcagc agaaaccagg acagcctcct 540
 aagctgctca ttacttgggc atctaccggg gaatccgggg tccctgaccg attcagtggc 600
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 gtttattact gtcagcaata ttattcctat ccgttgacgt tcggccaagg gaccaagggtg 720
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 gcatag 786

<210> 9
 <211> 13
 <212> PRT
 <213> PreS1 epitope at C-terminal of Tag-72pS1

<400> 9
 Gly Ala Asn Ala Asn Asn Pro Asp Trp Asp Phe Asn Pro
 1 5 10

<210> 10
 <211> 2871
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> ScFv-GaLV Env GP chimeric peptide (FvGEL199) DNA

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 atgagtccctg ggagctggaa aagactgac atcctcttaa gctgcgtatt cggcggcggc 120
 gggacgagtc tgcaaaataa gaacccccac cagcccatga ccctcacttg gcaggtactg 180
 tcccaaactg gagacgttgt ctgggatata aaggcagtc agcccccttg gacttggtgg 240

cccacactta aacctgatgt atgtgccttg gcggctagtc ttgagtcctg ggatatcccg	300
ggaaccgatg tctcgtcctc taaacgagtc agacctccgg actcagacta tactgccgct	360
tataagcaaa tcacctgggg agccataggg tgcagctacc ctcgggctag gactagaatg	420
gcaagctcta ccttctacgt atgtccccgg gatggccgga ccctttcaga agctagaagg	480
tgcggggggc tagaatccct atactgtaaa gaatgggatt gtgagaccac ggggaccggt	540
tattggctat ctaaatcctc aaaagacctc ataactgtaa aatgggacca aaatagcgga	600
ggtggtggca gccaggcca gctagtgcag tctggggctg aagtgaagaa gcctggggct	660
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cagaccggct ggtgtaaccc ccttaaaata gatttcacag acaaaggaaa attatccaag	1500
gactggataa cgggaaaaac ctggggatta agattctatg tgtctggaca tccaggcgta	1560

cagttcacca ttgccttaaa aatcaccaac atgccagctg tggcagtagg tctlgacctc	1620
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gccactgagt ctgctggct ttgtttggcc atgggcccc cttattatga agcaatagcc	1920
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aagctacccc tactgaggt ctcaggacac gggttgtgca taggaaagg tgcctttacc	2040
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<210> 11
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ScFv-GaLV Env GP chimeric ligand (FvGEL199)

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 20 25 30
 Leu Ser Cys Val Phe Gly Gly Gly Gly Thr Ser Leu Gln Asn Lys Asn
 35 40 45
 Pro His Gln Pro Met Thr Leu Thr Trp Gln Val Leu Ser Gln Thr Gly
 50 55 60
 Asp Val Val Trp Asp Thr Lys Ala Val Gln Pro Pro Trp Thr Trp Trp
 65 70 75 80
 Pro Thr Leu Lys Pro Asp Val Cys Ala Leu Ala Ala Ser Leu Glu Ser
 85 90 95
 Trp Asp Ile Pro Gly Thr Asp Val Ser Ser Ser Lys Arg Val Arg Pro
 100 105 110
 Pro Asp Ser Asp Tyr Thr Ala Ala Tyr Lys Gln Ile Thr Trp Gly Ala
 115 120 125
 Ile Gly Cys Ser Tyr Pro Arg Ala Arg Thr Arg Met Ala Ser Ser Thr
 130 135 140
 Phe Tyr Val Cys Pro Arg Asp Gly Arg Thr Leu Ser Glu Ala Arg Arg
 145 150 155 160
 Cys Gly Gly Leu Glu Ser Leu Tyr Cys Lys Glu Trp Asp Cys Glu Thr
 165 170 175

Thr Gly Thr Gly Tyr Trp Leu Ser Lys Ser Ser Lys Asp Leu Ile Thr
 180 185 190

Val Lys Trp Asp Gln Asn Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
 195 200 205

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 210 215 220

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His Ala Ile His Trp
 225 230 235 240

Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met Gly Tyr Phe Ser
 245 250 255

Pro Gly Asn Asp Asp Phe Lys Tyr Ser Gln Lys Phe Gln Gly Arg Val
 260 265 270

Thr Ile Thr Ala Asp Lys Ser Ala Ser Thr Ala Tyr Met Glu Leu Ser
 275 280 285

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Leu
 290 295 300

Asp Met Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
 305 310 315 320

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
 325 330 335

Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg
 340 345 350

Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn
 355 360 365

Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 370 375 380

Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp
 385 390 395 400

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser

	405		410		415										
Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Tyr
	420							425					430		
Ser	Tyr	Pro	Leu	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Ala
	435						440					445			
Ala	Ala	Gly	Ala	Asn	Ala	Asn	Asn	Pro	Asp	Trp	Asp	Phe	Asn	Pro	Ala
	450					455					460				
Ala	Gly	Gly	Gly	Gly	Ser	Glu	Trp	Thr	Gln	Lys	Phe	Gln	Gln	Cys	His
465					470					475				480	
Gln	Thr	Gly	Trp	Cys	Asn	Pro	Leu	Lys	Ile	Asp	Phe	Thr	Asp	Lys	Gly
				485					490					495	
Lys	Leu	Ser	Lys	Asp	Trp	Ile	Thr	Gly	Lys	Thr	Trp	Gly	Leu	Arg	Phe
	500							505					510		
Tyr	Val	Ser	Gly	His	Pro	Gly	Val	Gln	Phe	Thr	Ile	Arg	Leu	Lys	Ile
	515					520						525			
Thr	Asn	Met	Pro	Ala	Val	Ala	Val	Gly	Pro	Asp	Leu	Val	Leu	Val	Glu
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Gln	Gly	Pro	Pro	Arg	Thr	Ser	Leu	Ala	Leu	Pro	Pro	Pro	Leu	Pro	Pro
545				550						555				560	
Arg	Glu	Ala	Pro	Pro	Pro	Ser	Leu	Pro	Asp	Ser	Asn	Ser	Thr	Ala	Leu
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Ala	Thr	Ser	Ala	Gln	Thr	Pro	Thr	Val	Arg	Lys	Thr	Ile	Val	Thr	Leu
		580						585					590		
Asn	Thr	Pro	Pro	Pro	Thr	Thr	Gly	Asp	Arg	Leu	Phe	Asp	Leu	Val	Gln
	595						600					605			
Gly	Ala	Phe	Leu	Thr	Leu	Asn	Ala	Thr	Asn	Pro	Gly	Ala	Thr	Glu	Ser
	610					615					620				
Cys	Trp	Leu	Cys	Leu	Ala	Met	Gly	Pro	Pro	Tyr	Tyr	Glu	Ala	Ile	Ala
625				630						635				640	

Ser Ser Gly Glu Val Ala Tyr Ser Thr Asp Leu Asp Arg Cys Arg Trp
645 650 655

Gly Thr Gln Gly Lys Leu Thr Leu Thr Glu Val Ser Gly His Gly Leu
660 665 670

Cys Ile Gly Lys Val Pro Phe Thr His Gln His Leu Cys Asn Gln Thr
675 680 685

Leu Ser Ile Asn Ser Ser Gly Asp His Gln Tyr Leu Leu Pro Ser Asn
690 695 700

His Ser Trp Trp Ala Cys Ser Thr Gly Leu Thr Pro Cys Leu Ser Thr
705 710 715 720

Ser Val Phe Asn Gln Thr Arg Asp Phe Cys Ile Gln Val Gln Leu Ile
725 730 735

Pro Arg Ile Tyr Tyr Tyr Pro Glu Glu Val Leu Leu Gln Ala Tyr Asp
740 745 750

Asn Ser His Pro Arg Thr Lys Arg Glu Ala Val Ser Leu Thr Leu Ala
755 760 765

Val Leu Leu Gly Leu Gly Ile Thr Ala Gly Ile Gly Thr Gly Ser Thr
770 775 780

Ala Leu Ile Lys Gly Pro Ile Asp Leu Gln Gln Gly Leu Thr Ser Leu
785 790 795 800

Gln Ile Ala Ile Asp Ala Asp Leu Arg Ala Leu Gln Asp Ser Val Ser
805 810 815

Lys Leu Glu Asp Ser Leu Thr Ser Leu Ser Glu Val Val Leu Gln Asn
820 825 830

Arg Arg Gly Leu Asp Leu Leu Phe Leu Lys Glu Gly Gly Leu Cys Ala
835 840 845

Ala Leu Lys Glu Glu Cys Cys Phe Tyr Ile Asp His Ser Gly Ala Val
850 855 860

Arg Asp Ser Met Lys Lys Leu Lys Glu Lys Leu Asp Lys Arg Gln Leu
865 870 875 880

Glu Arg Gln Lys Ser Gln Asn Trp Tyr Glu Gly Trp Phe Asn Asn Ser
 885 890 895

Pro Trp Phe Thr Thr Leu Leu Ser Thr Ile Ala Gly Pro Leu Leu Leu
 900 905 910

Leu Leu Leu Leu Leu Ile Leu Gly Pro Cys Ile Ile Asn Lys Leu Val
 915 920 925

Gln Phe Ile Asn Asp Arg Ile Ser Ala Val Lys Ile Leu Val Leu Arg
 930 935 940

Gln Lys Tyr Gln Ala Leu Glu Asn Glu Gly Asn Leu
 945 950 955